

REMARKS

The Office Action and the cited and applied references have been carefully reviewed. Claims 13, 28 and 35 are allowed. Claims 1-5, 7-10, 12-15, 17-20, 23, 24, 27, 28, and 32-40 presently appear in this application and define patentable subject matter warranting their allowance. Reconsideration and allowance are hereby respectfully solicited.

The feature of "having up to 30 nucleotides in length" for the single stranded RNA molecule as recited in amended claim 23 finds support in the specification on page 14, lines 19-21, where it is disclosed that sequences shorter than 17 or 30 nucleotides may be used.

New claim 39 recites the feature "having 100% complementarity" which finds implicit support on page 14 of the specification, lines 23-25. While this disclosure indicates that non-complementary bases can be tolerated, it would be clear to those of skill in the art that the optimal situation is where the antisense molecule has 100% complementarity.

Claims 19 and 20 have been objected to because of informalities. Appropriate corrections are made, thereby obviating these objections.

Claims 1, 2, 11-12, 14-15, 16-20, 24, and 31-32 have been rejected under 35 U.S.C. §112, first paragraph because the examiner states that the specification, while being enabling for

SEQ ID NO:2 and fragments which are capable of inducing cell death, does not reasonably provide enablement for at least 85% homologs of said fragments which are capable of inducing cell death shown in claim 1(D), or 85% or higher homologs of fragments of claim 1 (E) wherein said fragment can inhibit the ability of polypeptides of claim 1(A) or (B) to induce cell death shown in claim 1(F). This rejection is believed to be obviated by the amendments to the claims.

Claims 1, 8-9, 11, 12, and 27 have been rejected under 35 U.S.C. §102(b) or 102(a) as being anticipated by Deiss or Akira. This rejection is obviated by the amendment of the claims to recite "at least 90% sequence identity". Even if one of skill in the art would interpret the sequence alignments to show 83.7% or 82.4% "sequence identity" to the sequences in Deiss and Akira (which applicants have previously argued that one of skill in the art would not), the sequences of Deiss and Akira are clearly not encompassed by a polypeptide having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2 as now recited in the claims.

Reconsideration and withdrawal of the rejection are therefore respectfully requested.

Claims 11 and 6 have been rejected under 35 U.S.C. §102(e) as being anticipated by Akira et al., U.S. Patent No.

5,958,748. This rejection is obviated by the cancellation without prejudice of rejected claims 6 and 11.

Claim 23 has been rejected under 35 U.S.C. §102(b) as being anticipated by Marra et al. This rejection is obviated by the amendment to claim 23 to recite that the single stranded RNA has up to 30 nucleotides in length, or in other words, a maximum of 30 nucleotides. Marra's mRNA is 869 nucleotides in length. New claim 39 is not subject to this rejection because it recites 100% complementarity.

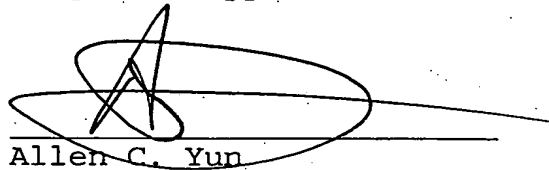
Reconsideration and withdrawal of the rejection are therefore respectfully requested.

In view of the above, the claims comply with 35 U.S.C. §112 and define patentable subject matter warranting their allowance. Favorable consideration and earnestly urged.

Respectfully submitted,

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A handwritten signature in black ink, appearing to be 'Allen C. Yun', is written over a horizontal line. The signature is stylized with a large loop and a crossbar.

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